



SEQUENCE LISTING

<110> Moon, Chulso
Mao, Li

<120> DAP-Kinase and HOXA9, Two Human Genes Associated with Genesis,
Progression, and Aggressiveness of Non-Small Cell Lung Cancer

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<140> 10/045,400

<141> 2001-11-29

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 Ile Met Leu Leu Asp Arg Asn Val Pro Lys Pro Arg Ile Lys Ile Ile
 145 150 155 160
 Asp Phe Gly Leu Ala His Lys Ile Asp Phe Gly Asn Glu Phe Lys Asn
 165 170 175
 Ile Phe Gly Thr Pro Glu Phe Val Ala Pro Glu Ile Val Asn Tyr Glu
 180 185 190
 Pro Leu Gly Leu Glu Ala Asp Met Trp Ser Ile Gly Val Ile Thr Tyr
 195 200 205
 Ile Leu Leu Ser Gly Ala Ser Pro Phe Leu Gly Asp Thr Lys Gln Glu
 210 215 220
 Thr Leu Ala Asn Val Ser Ala Val Asn Tyr Glu Phe Glu Asp Glu Tyr
 225 230 235 240
 Phe Ser Asn Thr Ser Ala Leu Ala Lys Asp Phe Ile Arg Arg Leu Leu
 245 250 255
 Val Lys Asp Pro Lys Lys Arg Met Thr Ile Gln Asp Ser Leu Gln His
 260 265 270
 Pro Trp Ile Lys Pro Lys Asp Thr Gln Gln Ala Leu Ser Arg Lys Ala
 275 280 285
 Ser Ala Val Asn Met Glu Lys Phe Lys Lys Phe Ala Ala Arg Lys Lys
 290 295 300
 Trp Lys Gln Ser Val Arg Leu Ile Ser Leu Cys Gln Arg Leu Ser Arg
 305 310 315 320
 Ser Phe Leu Ser Arg Ser Asn Met Ser Val Ala Arg Ser Asp Asp Thr
 325 330 335
 Leu Asp Glu Glu Asp Ser Phe Val Met Lys Ala Ile Ile His Ala Ile
 340 345 350

Asn Asp Asp Asn Val Pro Gly Leu Gln His Leu Leu Gly Ser Leu Ser
355 360 365

Asn Tyr Asp Val Asn Gln Pro Asn Lys His Gly Thr Pro Pro Leu Leu
370 375 380

Ile Ala Ala Gly Cys Gly Asn Ile Gln Ile Leu Gln Leu Leu Ile Lys
385 390 395 400

Arg Gly Ser Arg Ile Asp Val Gln Asp Lys Gly Gly Ser Asn Ala Val
405 410 415

Tyr Trp Ala Ala Arg His Gly His Val Asp Thr Leu Lys Phe Leu Ser
420 425 430

Glu Asn Lys Cys Pro Leu Asp Val Lys Asp Lys Ser Gly Glu Met Ala
435 440 445

Leu His Val Ala Ala Arg Tyr Gly His Ala Asp Val Ala Gln Val Thr
450 455 460

Cys Ala Ala Ser Ala Gln Ile Pro Ile Ser Arg Thr Lys Glu Glu Glu
465 470 475 480

Thr Pro Leu His Cys Ala Ala Trp His Gly Tyr Tyr Ser Val Ala Lys
485 490 495

Ala Leu Cys Glu Ala Gly Cys Asn Val Asn Ile Lys Asn Arg Glu Gly
500 505 510

Glu Thr Pro Leu Leu Thr Ala Ser Ala Arg Gly Tyr His Asp Ile Val
515 520 525

Glu Cys Leu Ala Glu His Gly Ala Asp Leu Asn Ala Cys Asp Lys Asp
530 535 540

Gly His Ile Ala Leu His Leu Ala Val Arg Arg Cys Gln Met Glu Val
545 550 555 560

Ile Lys Thr Leu Leu Ser Gln Gly Cys Phe Val Asp Tyr Gln Asp Arg
565 570 575

His Gly Asn Thr Pro Leu His Val Ala Cys Lys Asp Gly Asn Met Pro
580 585 590

Ile	Val	Val	Ala	Leu	Cys	Glu	Ala	Asn	Cys	Asn	Leu	Asp	Ile	Ser	Asn	595	600	605
Lys	Tyr	Gly	Arg	Thr	Pro	Leu	His	Leu	Ala	Ala	Asn	Asn	Gly	Ile	Leu	610	615	620
Asp	Val	Val	Arg	Tyr	Leu	Cys	Leu	Met	Gly	Ala	Ser	Val	Glu	Ala	Leu	625	630	635
Thr	Thr	Asp	Gly	Lys	Thr	Ala	Glu	Asp	Leu	Ala	Arg	Ser	Glu	Gln	His	645	650	655
Glu	His	Val	Ala	Gly	Leu	Leu	Ala	Arg	Leu	Arg	Lys	Asp	Thr	His	Arg	660	665	670
Gly	Leu	Phe	Ile	Gln	Gln	Leu	Arg	Pro	Thr	Gln	Asn	Leu	Gln	Pro	Arg	675	680	685
Ile	Lys	Leu	Lys	Leu	Phe	Gly	His	Ser	Gly	Ser	Gly	Lys	Thr	Thr	Leu	690	695	700
Val	Glu	Ser	Leu	Lys	Cys	Gly	Leu	Leu	Arg	Ser	Phe	Phe	Arg	Arg	Arg	705	710	715
Arg	Pro	Arg	Leu	Ser	Ser	Thr	Asn	Ser	Ser	Arg	Phe	Pro	Pro	Ser	Pro	725	730	735
Leu	Ala	Ser	Lys	Pro	Thr	Val	Ser	Val	Ser	Ile	Asn	Asn	Leu	Tyr	Pro	740	745	750
Gly	Cys	Glu	Asn	Val	Ser	Val	Arg	Ser	Arg	Ser	Met	Met	Phe	Glu	Pro	755	760	765
Gly	Leu	Thr	Lys	Gly	Met	Leu	Glu	Val	Phe	Val	Ala	Pro	Thr	His	His	770	775	780
Pro	His	Cys	Ser	Ala	Asp	Asp	Gln	Ser	Thr	Lys	Ala	Ile	Asp	Ile	Gln	785	790	795
Asn	Ala	Tyr	Leu	Asn	Gly	Val	Gly	Asp	Phe	Ser	Val	Trp	Glu	Phe	Ser	805	810	815
Gly	Asn	Pro	Val	Tyr	Phe	Cys	Cys	Tyr	Asp	Tyr	Phe	Ala	Ala	Asn	Asp			

820	825	830
Pro Thr Ser Ile His Val Val Val Phe Ser Leu Glu Glu Pro Tyr Glu		
835	840	845
Ile Gln Leu Asn Pro Val Ile Phe Trp Leu Ser Phe Leu Lys Ser Leu		
850	855	860
Val Pro Val Glu Glu Pro Ile Ala Phe Gly Gly Lys Leu Lys Asn Pro		
865	870	880
Leu Gln Val Val Leu Val Ala Thr His Ala Asp Ile Met Asn Val Pro		
	885	890
Arg Pro Ala Gly Gly Glu Phe Gly Tyr Asp Lys Asp Thr Ser Leu Leu		
	900	910
Lys Glu Ile Arg Asn Arg Phe Gly Asn Asp Leu His Ile Ser Asn Lys		
	915	925
Leu Phe Val Leu Asp Ala Gly Ala Ser Gly Ser Lys Asp Met Lys Val		
	930	940
Leu Arg Asn His Leu Gln Glu Ile Arg Ser Gln Ile Val Ser Val Cys		
	945	955
Pro Pro Met Thr His Leu Cys Glu Lys Ile Ile Ser Thr Leu Pro Ser		
	965	970
Trp Arg Lys Leu Asn Gly Pro Asn Gln Leu Met Ser Leu Gln Gln Phe		
	980	985
Val Tyr Asp Val Gln Asp Gln Leu Asn Pro Leu Ala Ser Glu Glu Asp		
	995	1000
Leu Arg Arg Ile Ala Gln Gln Leu His Ser Thr Gly Glu Ile Asn		
	1010	1015
Ile Met Gln Ser Glu Thr Val Gln Asp Val Leu Leu Leu Asp Pro		
	1025	1030
Arg Trp Leu Cys Thr Asn Val Leu Gly Lys Leu Leu Ser Val Glu		
	1040	1045
		1050

Thr	Pro	Arg	Ala	Leu	His	His	Tyr	Arg	Gly	Arg	Tyr	Thr	Val	Glu
1055						1060					1065			
Asp	Ile	Gln	Arg	Leu	Val	Pro	Asp	Ser	Asp	Val	Glu	Glu	Leu	Leu
1070						1075					1080			
Gln	Ile	Leu	Asp	Ala	Met	Asp	Ile	Cys	Ala	Arg	Asp	Leu	Ser	Ser
1085						1090					1095			
Gly	Thr	Met	Val	Asp	Val	Pro	Ala	Leu	Ile	Lys	Thr	Asp	Asn	Leu
1100						1105					1110			
His	Arg	Ser	Trp	Ala	Asp	Glu	Glu	Asp	Glu	Val	Met	Val	Tyr	Gly
1115						1120					1125			
Gly	Val	Arg	Ile	Val	Pro	Val	Glu	His	Leu	Thr	Pro	Phe	Pro	Cys
1130						1135					1140			
Gly	Ile	Phe	His	Lys	Val	Gln	Val	Asn	Leu	Cys	Arg	Trp	Ile	His
1145						1150					1155			
Gln	Gln	Ser	Thr	Glu	Gly	Asp	Ala	Asp	Ile	Arg	Leu	Trp	Val	Asn
1160						1165					1170			
Gly	Cys	Lys	Leu	Ala	Asn	Arg	Gly	Ala	Glu	Leu	Leu	Val	Leu	Leu
1175						1180					1185			
Val	Asn	His	Gly	Gln	Gly	Ile	Glu	Val	Gln	Val	Arg	Gly	Leu	Glu
1190						1195					1200			
Thr	Glu	Lys	Ile	Lys	Cys	Cys	Leu	Leu	Leu	Asp	Ser	Val	Cys	Ser
1205						1210					1215			
Thr	Ile	Glu	Asn	Val	Met	Ala	Thr	Thr	Leu	Pro	Gly	Leu	Leu	Thr
1220						1225					1230			
Val	Lys	His	Tyr	Leu	Ser	Pro	Gln	Gln	Leu	Arg	Glu	His	His	Glu
1235						1240					1245			
Pro	Val	Met	Ile	Tyr	Gln	Pro	Arg	Asp	Phe	Phe	Arg	Ala	Gln	Thr
1250						1255					1260			
Leu	Lys	Glu	Thr	Ser	Leu	Thr	Asn	Thr	Met	Gly	Gly	Tyr	Lys	Glu
1265						1270					1275			

Ser Phe Ser Ser Ile Met Cys Phe Gly Cys His Asp Val Tyr Ser
1280 1285 1290

Gln Ala Ser Leu Gly Met Asp Ile His Ala Ser Asp Leu Asn Leu
1295 1300 1305

Leu Thr Arg Arg Lys Leu Ser Arg Leu Leu Asp Pro Pro Asp Pro
1310 1315 1320

Leu Gly Lys Asp Trp Cys Leu Leu Ala Met Asn Leu Gly Leu Pro
1325 1330 1335

Asp Leu Val Ala Lys Tyr Asn Thr Asn Asn Gly Ala Pro Lys Asp
1340 1345 1350

Phe Leu Pro Ser Pro Leu His Ala Leu Leu Arg Glu Trp Thr Thr
1355 1360 1365

Tyr Pro Glu Ser Thr Val Gly Thr Leu Met Ser Lys Leu Arg Glu
1370 1375 1380

Leu Gly Arg Arg Asp Ala Ala Asp Leu Leu Leu Lys Ala Ser Ser
1385 1390 1395

Val Phe Lys Ile Asn Leu Asp Gly Asn Gly Gln Glu Ala Tyr Ala
1400 1405 1410

Ser Ser Cys Asn Ser Gly Thr Ser Tyr Asn Ser Ile Ser Ser Val
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Val Ser Arg
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48

cg	cg	cg	gc	ag	ca	gc	tc	cg	gc	gc	ca	ga	ct	gc	gg	96	
Arg	Arg	Arg	Ala	Arg	His	Ala	Ser	Arg	Ala	Ala	Pro	Glu	Leu	Val	Gly		
			20					25					30				
ga	tt	gg	ag	tt	ct	tt	tg	gg	tc	ac	tt	ct	tc	gc	ac	gg	144
Asp	Leu	Gly	Ser	Phe	Leu	Leu	Gly	Ser	Thr	Phe	Leu	Ser	Thr	Gly			
		35					40				45						
ac	ca	ct	cc	tt	at	ac	tc	gt	ga	at	gc	tc	ag	ta	ct		192
Thr	Thr	Leu	Pro	Phe	Ile	Thr	Ser	Val	Glu	Ile	Val	Ser	Arg	Tyr	Leu		
		50				55					60						
tg	gc	cg	gg	tc	gg	cg	gc	gg	ca	ca	gg	cc	gg	cg	gc		240
Cys	Ala	Arg	Gly	Ser	Gly	Arg	Ala	Gly	His	His	Gly	Pro	Gly	Arg	Ala		
		65				70				75					80		
ag	cc	gc	gt	gc	ac	tc	gc	tt	cc	gc	ca	ga	cc	cg	gc		288
Arg	Pro	Ala	Val	Ala	Thr	Ser	Ala	Phe	Pro	Ala	Gln	Glu	Pro	Arg	Val		
			85					90						95			
tt	ct	cg	ag	gc	tt	cc	gc	gg	cg	ct	tc	cc	tc	ac	ca		336
Phe	Leu	Arg	Ser	Ala	Leu	Pro	Ala	Gly	Arg	Leu	Ser	Pro	Ser	Thr	Thr		
			100					105					110				
ca	ct	ca	ct	gc	ac	gc	ga	aa	ca	gc	gc	aa	tg	ct	ca		384
His	Leu	His	Leu	Val	Thr	Ala	Asp	Asn	Pro	Ala	Ala	Asn	Trp	Leu	His		
			115				120					125					
gc	cg	tc	ac	cg	aa	aa	cg	tg	cc	ta	ac	aa	ca	ca	ac		432
Ala	Arg	Ser	Thr	Arg	Lys	Lys	Arg	Cys	Pro	Tyr	Thr	Lys	His	Gln	Thr		
			130				135				140						
ct	ga	ct	ga	aa	ga	tt	ct	tc	aa	at	ta	ct	ac	ag	ga		480
Leu	Glu	Leu	Glu	Lys	Glu	Phe	Leu	Phe	Asn	Met	Tyr	Leu	Thr	Arg	Asp		
		145				150				155					160		
cg	ag	ta	ga	gt	gc	ca	ct	ct	aa	ct	ac	ga	ag	ca	gc		528
Arg	Arg	Tyr	Glu	Val	Ala	Arg	Leu	Leu	Asn	Leu	Thr	Glu	Arg	Gln	Val		
			165						170					175			
aa	at	tg	tt	ca	aa	cg	ag	at	aa	at	aa	aa	at	aa	aa		576
Lys	Ile	Trp	Phe	Gln	Asn	Arg	Arg	Met	Lys	Met	Lys	Lys	Ile	Asn	Lys		
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ga	ca	gc	aa	ga	ga	tg											597
Asp	Arg	Ala	Lys	Asp	Glu												
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Met	Ala	Gly	Phe	Ser	Pro	Trp	Arg	Arg	Arg	Gln	Arg	Arg	Arg	Arg	Arg		
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1																	

Arg Arg Arg Ala Arg His Ala Ser Arg Ala Ala Pro Glu Leu Val Gly
20 25 30

Asp Leu Gly Ser Phe Leu Leu Leu Gly Ser Thr Phe Leu Ser Thr Gly
35 40 45

Thr Thr Leu Pro Phe Ile Thr Ser Val Glu Ile Val Ser Arg Tyr Leu
50 55 60

Cys Ala Arg Gly Ser Gly Arg Ala Gly His His Gly Pro Gly Arg Ala
65 70 75 80

Arg Pro Ala Val Ala Thr Ser Ala Phe Pro Ala Gln Glu Pro Arg Val
85 90 95

Phe Leu Arg Ser Ala Leu Pro Ala Gly Arg Leu Ser Pro Ser Thr Thr
100 105 110

His Leu His Leu Val Thr Ala Asp Asn Pro Ala Ala Asn Trp Leu His
115 120 125

Ala Arg Ser Thr Arg Lys Lys Arg Cys Pro Tyr Thr Lys His Gln Thr
130 135 140

Leu Glu Leu Glu Lys Glu Phe Leu Phe Asn Met Tyr Leu Thr Arg Asp
145 150 155 160

Arg Arg Tyr Glu Val Ala Arg Leu Leu Asn Leu Thr Glu Arg Gln Val
165 170 175

Lys Ile Trp Phe Gln Asn Arg Arg Met Lys Met Lys Lys Ile Asn Lys
180 185 190

Asp Arg Ala Lys Asp Glu
195